Appl. No. 09/944,049 Amdt. dated January 27, 2004 Response to Notice of Allowance October 29, 2003 **PATENT**

Amendments to the Drawings:

The attached sheets of drawings include changes to Figs. 1A, 1B, Fig. 2 (both pages), and Figs. 3-7. These sheets, which include Figs. 1A, 1B, 2A-2C, 3, 4A and 4B, and 5-7 replace the original sheets including Figs. 1A, 1B, Fig. 2 (both pages), and Figs. 3-7.

Attachment: Replacement Sheets



```
VHLE
        1 ATGACACCGACGACGACGACCGCGGAACTCACG
                                                  33
VHL
         ACGGAGTTTGACTACGACGATGAAGCGACTCCC
                                                  66
VHLE
         TGTGTCCTCACCGACGTGCTTAATCAGTCGAAG
                                                  99
VHLE
         CCAGTCACGTTGTTTCTGTACGGCGTTGTCTTT
                                                 132
VHLE
       133 CTCTTCGGTTCCATCGGCAACTTCTTGGTGATC
                                                 165
VHL/E
         TTCACCATCACCTGGCGACGTCGGATTCAATGT
                                                 198
VHL/E
         TCCGGCGATGTTTACTTTATCAACCTCGCGGCC
                                                 231
VHL/E
      232 GCCGATTTGCTTTTCGTTTGTACACTACCTCTG
                                                 264
VHL/E
      265
         TGGATGCAATACCTCCTAGATCACAACTCCCTA
                                                 297
VHL/E
         GCCAGCGTGCCGTGTACGTTACTCACTGCCTGT
      298
                                                 330
VHL/E
         TTCTACGTGGCTATGTTTGCCAGTTTGTGTTTT
      331
                                                 363
VHL/E
         ATCACGGAGATTGCACTCGATCGCTACTACGCT
      364
                                                 396
VHL/E
         ATTGTTTACATGAGATATCGGCCTGTAAAACAG
                                                 429
VHL/E
         GCCTGCCTTTTCAGTATTTTTTTGGTGGATCTTT
                                                 462
VHL/E
         GCCGTGATCATCGCCATTCCACACTTTATGGTG
                                                 495
VHL/E
         GTGACCAAAAAAGACAATCAATGTATGACCGAC
                                                 528
VHL/E
         TACGACTACTTAGAGGTCAGTTACCCGATCATC
      529
                                                 561
VHL/E
         CTCAACGTAGAACTCATGCTCGGTGCTTTCGTG
                                                 594
VHL
         ATCCCGCTCAGTGTCATCAGCTACTGCTACTAC
                                                 627
VHL/E
         CGCATTTCCAGAATCGTTGCGGTGTCTCAGTCG
                                                 660
VHL/E
         CGCCACAAAGGCCGCATTGTACGGGTACTTATA
      661
                                                 693
VHL/E
         GCGGTCGTGCTTGTCTTTATCATCTTTTGGCTG
      694
                                                 726
VHL/E
      727 CCGTACCACCTGACGCTGTTTGTGGACACGTTG
                                                 759
VHL/E
         AAACTGCTCAAATGGATCTCCAGCAGCTGCGAG
                                                 792
VHL/E
         TTCGAAAAATCACTCAAGCGCGCGCTCATCTTG
                                                 825
VHL/E
         ACCGAGTCACTCGCCTTTTGTCACTGTTGTCTC
      826
                                                 858
         AATCCGCTGCTGTACGTCTTCGTGGGCACCAAG
VHL/E
                                                 891
VHL/E
         TTTCGGCAAGAACTGCACTGTCTGCTGGCCGAG
                                                 924
VHLE
         TTTCGCCAGCGACTGTTTTCCCGCGATGTATCC
      925
                                                 957
VHLE
         TGGTACCACAGCATGAGCTTTTCGCGTCGGAGC
                                                 990
VHL
         TCGCCGAGCCGAAGAGAGACGTCTTCCGACACG
                                                1023
         CTGTCCGACGAGGCGTGTCGCGTCTCACAAATT
VHL/E
                                                 1056
VHL/E
         ATACCGTAA
      1057
                                                1065
```



VHL/E	1	MTPTTTTAELTTEFDYDDEATPCVLTDVLNQSK	33
VHL/E	34	<u>PVTLF</u> LYGVVFLFGSIGNFLVIFTITWRRRIQC	66
VHL/E	- 67	SGDVYFINLAAADLLFVCTLPLWMQYLLDHNSL	.99
VHL/E	100	ASVPCTLLTACFYVAMFASLCFITEIALDRYYA	132
VHL/E	133	IVYMRYRPVKQACLFSIFWWIFAVIIAIPHFMV	165
VHL/E	166	VTKKDNQCMTDYDYLEVSYPIILNVELMLGAFV	198
VHL/E	199	IPLSVISYCYYRISRIVAVSQSRHKGRIVRVLI	231
VHLYE	232	AVVLVFIIFWLPYHLTLFVDTLKLLKWISSSCE	264
VHL/E	265	FEKSLKRALILTESLAFCHCCLNPLLYVFVGTK	297
VHL/E	298	FRQELHCLLAEFRQRLFSRDVSWYHSMSFSRRS	330
VHL/E	331	SPSRRETSSDTLSDEACRVSQIIP	354



	ĪT	
rhesus US28.1 1 M		- 1
rhesus US28.2 1 MTN	Ā]	- 4
rhesus US28.3 1 MTN	<u>T</u> -	- 4
rhesus US28.4 1 M	 • • • • • • • • • • • • • • • • • • •	- 0
rhesus US28.5 1 MTT	TT MS AT T NSSTT PQASST TMT TKTST PGN	N 32
human US28 6	-TTAELTT	- 12
		-
rhesus US28.5 83 TTT(GTTSTLTTISTTSNATSIT SNLSTTGNQ ⁻	T 64
	GH	
	NN1	
rhesus US28.4 1 ·	NSSQHNISV FLS	- 15
rhesus US28.5 65 ATTI	NATTFS STLTTSTN I SST FSTVSTVA S N.A	A 96
rhesus US28.5 97 T C N S	STITTN ITTAFTTAANTT ASSLTSIVTSL	_ 128
		_
human US28 13	EFDYDEDATPCMFTDVLNQSKPVTL	_ 37
rhesus US28.1 9 NVTI	LNA S A PSRY I A I	23
rhesus US28.2 10 NESI	LASYG IAPAATI	24
	FET FK I TRPVA I	26
rhesus US28.4 22		21
rhesus US28.5 ₁₂₉ ATT	IETTSFDYDESAEACNLTDIVHTTRSVTV	/ 160



```
human US28
              rhesus US28.1 24
             AMYSIVICI GLVGNLLLCIVLVK - KRKLRYSS
                                                             54
rhesus US28.2 25
              T|LYSIA|G|ICGVTGNL|L|ILLVLFT|-|RR|IHW|F
                                                             55
rhesus US28.3 27
              SAYTVLVVIGLLGNI|V|LLSVLVV|-KRKLKF
                                                             57
               - YTCVFLFGILGHFYLYWKNHQRRHRTNS
rhesus US28.4 22
                                                             51
rhesus US28.5 61
              TFYTIIFILGLLGNF|-|LVLMTIIW/NRRISIF/M/V|
                                                             191
             D V Y F I N L A A A D L L F V C T L P L W M Q Y L L D H N S L A
human US28
                                                             100
             DVYFFHASMADLVSTVMLPLWLHYVLNFAQ
rhesus US28.1 55
                                                             86
rhesus US28.2 56.
             DIYYLNMIFTDFLVFITLPAWVYYLLNYTQLS
                                                             87
rhesus US28.3 58
             DIYFFNASLADVFAVCMLPAWVNYAL DSTQ
                                                             89
             DVLFRHLMITEEVFTLTIPVWAYHLTTHGN
rhesus US28.4 52
                                                             83
rhesus US28.5192
             |EIYFVNLAISDLMFVCTLPFWI|M|YL
                                                             223
human US28 101
             SVPCTLLTACFYVAMFASLCFITEIALDRY
                                                             132
rhesus US28.1 87
              RIGACISFSVTFYVPLFVQAWLLISIAMER
                                                             117
rhesus US28.2 88
              HYACIALSF V FYVS I FI QAD F MV A VA I ER |-
                                                             118
              K|FSCITFTFGFYVSLFI|QAWMLI|L|VTLER
rhesus US28.3 90
                                                             120
             |GSWCRSLTFVFYLTVFA|RAFFYL|L|LIWDR|-
rhesus US28.4 84
                                                             114
rhesus US28.5 24
              HASCVAMTA I FYCAL FASTV F L L
                                                             255
human US28 133
                 YMRYRPVKQ-----ACL FS
                                                             157
rhesus US28.1118
             NLVWMAPISVK---TAFKHCIGT
                                                             143
             SIL VKNKPLISIVK - - - KASVISCACII - - - | WIIVII
rhesus US28.2119
                                                             144
              SILVWIAPITIRINI---KAIANCVLIF
rhesus US28.3<sub>121</sub>
                                                             146
rhesus US28.4115
              V I I CRHPLP VINILNYS Q V IIGI- - - | LISIVWI- - | L V A V
                                                             141
rhesus US28.5256
              I L LGTEKAN RRLLRNAVSGCM LM
                                                             284
human US28 158
                                                             186
rhesus US28.1144
             VAISIPMYAYRNSHIDEHEICHLGNIYTIWHIINEIPLIHIT
                                                             175
                     YMF|RS|QHE|TIN|S|C|||LG|N|Y|T|W|H|M|N|SP|FR|T
rhesus US28.2145
                                                             176
rhesus US28.3147
                       |F|RN|E|SN|EHQC|I|M|RN|Y|T|W|S|V|GE|TW
                                                             178
rhesus US28.4142
             LSASPFSIFNG-SVKQCI-LGNMG-SIPSESSA
                                                             170
             LALPHFIFMKK-GTNVC-VAE YEPGL
rhesus US28.5285
                                                             314
```



```
human US28 187 I L NVEL MLGAFVIPLSVISYC YYRISRIVAVS
rhesus US28.1176 C MDMVII I VWT F LAPV L V TIII A S V K M- RRT T WG
                                                                    206
rhesus US28.2177 |T M|D|||S|I |N|I WS F V V P A V T T L L I A|R|R I Y|V - |C T S G|
                                                                    207
rhesus US28.3179 A L DFLI TLITFIMPVTIVLAL SFK MARWSTFG
                                                                    210
Thesus US28.4171 V L N L EV H L C S F WL P L I I M SANC YYQAKRRA S P D
                                                                    202
rhesus US28.5245 | FINTEV|N|LCTLVLPAAAI|I|YWYL
human US28 219 |QS|-|RHKGRIV|R|VLIAVVLVFII
rhesus US28.1207 NT-RLNEKNSDILIVLVVMTVF FWGPFNIVLV
                                                                    237
rhesus US28.2208 NK - KMNARA SIGLLEAMV I SMLF FGGILFNLNIF
                                                                    238
rhesus US28.3211 YR - NLT|SRT S|L|ILILILT VAAG FWGP|F|HL|F|MF
                                                                    241
rhesus US28.4203 Q - - LHE LYRCSLLITIITTYAI VWF PFHLALL
                                                                    232
rhesus US28.5347 ERLIRHIRILITS ILINII VLAVVI VFAL FWL PYNLML M
human US28 250 V D T LIKILI - ILIK WI SSSCEFERSLIKIR A LILTESLA
rhesus US28.1238 | I DINIILQRIYIY DITI-ITNICDVEIKIK HIIMAMISEA IV
rhesus US28.2239 RD - IVSDTS E DNKDCTYLKQE HFIRMVGVALV
                                                                    269
rhesus US28.3242 | I ENMAGQINY HIIQKDCWYLQDR HLCSLMTETLV
                                                                    273
rhesus US28.4233 | I D A L I S - I S H V E P S S A L H WA
                                                                    261
rhesus US28.5379 MYSUVH - MQ - I PWECS SEKILIRRS LIITES IA
human US28 281 F C H C C L N P L L Y V F V G T K F R Q E L H C L L A E F R Q R
rhesus US28.1269 YIFIRIGITAPI I YVGI SGRIFREE IIYIS LFIRRQPYN
rhesus US28.2270 YGRAIFNPF MYMCVSTRLRQE IKCLFMRTPYE
                                                                    301
rhesus US28.3274 | F L R SVF NPY I YMI I S Y K F RQ Q V R S L L K R T Q Y D
                                                                    305
rhesus US28.4262 | F V Y AG I SP L V Y FTICC P IT V RIFE L L MS L R P F F T -
                                                                    292
rhesus US28.5409 L S HCC I N P I I Y L L F G P R C R S E
human US28 313 L F SRDV SW- - YHSMS F SRRSS P SRRETSSDTL
                                                                    342
rhesus US28.1301 D|L|DP|DA|N - - - - - Q|F|M| I |E L T|S|Q |G|R S|R|NRN|A|R Q|S
                                                                    327
rhesus US28.2302 |T L|DAEHA
                                 - KILIMIVIN L KNR NAIN VPDIPIK
                                                                    325
rhesus US28.3306 |A L|DTTQ|L|
                                 - AET MQLKAK GVPVSDPA
                                                                    329
                        - WI SISKITIRRGIYIAPIKITIQPLNITPIDIE
rhesus US28.4293
rhesus US28.5441 L - CPHRS WS SIRAET VSI SI
human US28 343 S D E V CR V S Q I I P
                                                                    354
rhesus US28.1328 E S NVPQPEE C F W
                                                                    339
rhesus US28.2326 - - - - |PR|E|Y|E S|V|L
                                                                    333
rhesus US28.3380 - - - - | P|H D|C|E |C F|L
                                                                    337
rhesus US28.4318 DNKSPHLLN-
                                                                    327
rhesus US28.5472 D N|DV|HD E|L Q F L|I
                                                                    483
```



```
human UL78
          1 MSPSVEETTSVTESIMFAIVSFKHMGPFEGY
                                                      31
rhesus UL78
                                                      n
human UL78
          32 SMSADRAASDLLIGMFGSVSLVNLLTLIGCL
                                                      62
          1 - MITERVLAGILAGMTAAGSLVIILLAVV - - M
rhesus UL78
                                                      28
human UL78
          63 WVLRVTRP - - PVSVMIFTWNLVLSQFFSILA
rhesus UL78
          29 WLNMLDRAGMPMAVGHYTGNLVLTQVICIFS
                                                      59
human UL78
          92 TMLSKGI MLRGALNLSLCRLVLFVDDVGLYS
                                                      122
            - MLASKII V GMTSAA NMGF CG I V V FILEDT GLY
rhesus UL78
                                                      89
           TALFFLFLILDRLSAISMGRDLWHHE-TREN
human UL78 123
                                                      152
rhesus UL78
          90 VTSLLFMFMILDRMAAFLINGRLFWRQQTITKQ
                                                      120
human UL78 153 AGVALYAVAFAWV LSIVAAVPTAATGSL DYR
                                                      183
rhesus UL78 121 NLSTSVYIILFC WVLGMAAAVPNS
                                                      151
human UL78 184 WLGCQIPIQYAAVDLTIKMWFLLGAPMIAVL
                                                      214
rhesus UL78 152 RWERCE I PVSYAAI DMIVKL WFVLLAPVVLI
                                                      182
human UL78 215 ANVVELAYSDRRDHVWSYVGRVCTFMVTCLM
                                                      245
Thesus UL78 183 MAVIII QSSYHRDRERI WYYARRVFMFYTACF
                                                      213
human UL78 246 LFVPYYCFRV - - - - - LRGV - L QPASAAGTG
                                                      269
Thesus UL78 214 VMMVPYYFVRVMLSDFALVDIKTKTANSDEC
                                                      244
human UL78 270 FGIMDY WELATRTLLT MRLGILPLFIIAFFS
                                                      300
rhesus UL78 245 DSTFLDYLNMFTHVIYSFKLVVFALFIVLFC
                                                      275
human UL78 301 REPTKDLDDSFDYLVERCQQSCHGHFVRRLV
                                                      331
rhesus UL78 276 SINPMETLEECLERADAERQSRSEASQGERR
                                                      306
human UL78 332 QALKRAMYSVELAVCYFSTSVRDVAEAVKKS
                                                      362
rhesus UL78 307 LPINTCCIKLIELIKQYVSTLSKATRDNSGE
                                                      337
human UL78 363 SSRCYADATSAAVVVTITTITSEKATLVEHAEG
                                                      393
rhesus UL78 338 RANL PENAEDII GTT GSDQL PTEVT VT PN SSA
                                                      368
human UL78 394 MA SEMCPGTT I DVS AESSSVLCTDGENT VAS
                                                      424
rhesus UL78 369 VFSTGGTVSPV
                                                      379
                                                      431
human UL78 425 DATVTAL
```



```
H UL33
HUL33splice
RhUL33
RhUL33splice
          1 MAVTLRGGSPINFKLMIVSHRNRKFHEIRLFQ
                                                      32
H UL33
HUL33splice
                                                      23
RhUL33
                                                      1
RhUL33splice 33
            RSAIRPGGLWKPFFTTERETNSILHINTTCNV
                                                      64
H UL33
          2 TGPLFAIRTTEAVLNTFIIFVGGPLNAIVLIT
                                                      33
HUL33splice
         24
            TGPLFAIRTTEAVLNTFIIFVGGPLNAIVLIT
                                                      55
RhUL33
                                                      1
RhUL33splice 65 TDSLMAAKLGEALVNSALALFGTPLNAIVLVT
                                                      96
H UL33
           QLLTNRVLGYSTPTIYMTNLYSTNFLTLTVLP
                                                      65
HUL33splice
         56
            QLLTNRVLGYSTPTIYMTNLYSTNFLTLTVLP
                                                      87
RhUL33
                        -----TNLYSANFLILIVLP
                                                      16
RhUL33splice 97
            QLLANRVHGYSTPIIYMTNLYSANFLTLIVLP
                                                      128
H UL33
           PIVLSNOWLLPAGVASCKFLSVIYYSSCTVGF
                                                      97
           PIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF
HUL33splice
                                                      119
RhUL33
           PIVLS NOH LLPASAVTCKFLSLLYYSSCSVGF
         17
                                                      48
RhUL33splice 129 PIVLS NQH|LLPASAVTCKFLSLLYYSSCSVGF
                                                      160
H UL33
           ATVALIAADRYRVLHKRTYARQSYRSTYMILL
                                                      129
HUL33splice 120
           ATVALIAADRYRVLHKRTYARQSYRSTYMILL
                                                      151
           ATVALIAADRYRVIHRRTQARQSYRNTYMIVG
RhUL33
                                                      80
RhUL33splice 161 A T VAL I AADRYRV I HRRTQARQSYRNTYM I VG
                                                      192
H UL33
           L TWLAGL I FSVPAAVYTTVVMHHDANDTNNTN
         130
                                                      161
HUL33splice 152
           L'TWLAGLIFSVPAAVYTTVVMHHDANDTNNTN
                                                      183
            LTWLIGLICATPGGVYTTIVAHRDGE--SDAQ
RhUL33
         81
                                                      110
RhUL33splice 193
           L TWL I GL I CATPGGVYTT I VAHRDGE - - SDAQ
                                                      222
```



```
H UL33
          162 GHATCVLYFVAEEVHTVLLSWKVLLTMWWGAA
                                                            193
HUL33splice
             |GHATCVLYFVAEEVHTVLLSWKVLLTMVWGAA
                                                           215
RhUL33
             RIHINITCIMHIFAYDEVIY-IVLMVWKLLIVLVWGIV
                                                           141
             RIMNITCIMHIFAYDEVIY-IVLMVWKLLIVLVWGIV
RhUL33splice 223
                                                           253
H UL33
             PVIMMTWFYAFFYSTVQRTSLKQRSRTLTFVS
                                                           225
HUL33splice
         216 PV IMMTWFYAFFYSTVQRTSLKQRSRTLTFVS
                                                           247
          142 PVVMMSWFYAFFYNTVQRTAKKQQ-RTLKFVK
RhUL33
                                                           172
RhUL33splice 254 PVVMMSWFYAFFYNTVQRTAKKQQ-RTLKFVK
                                                           284
H UL33
            V L L I SF VAL QTPYVSL MI FNSYATTAWPM QCE
                                                           257
HUL33splice 248
             V L L I SF VAL QTPYVSL M I FNSYATTAWPM QCE
                                                           279
RhUL33
            VLLLSFILIQTPYVSIMIFNTYATVGWPMECA
          173
                                                           204
RhUL33splice 285 V L L L S F I I I Q T P Y V S I M I F N T Y A T V G W P M E C A
                                                           316
H UL33
            HLTLRRTIGTLARVVPHLHCLINPILYALLGH
                                                           289
HUL33splice 280 | HLTLRRTIGTLARVVPHLHCLINPILYALLGH
                                                           311
RhUL33
             DIL TIRIRRY I INTESRL VPNL HCMVNP I LYALMGN
                                                           236
RhUL33splice 317
             DIL TIRIRRV I INT FSRL VPNL HCMVNP I LYALMGN
            |DFLQRMRQCFRGQLLDRRAFLRSQNNQRATAE
H UL33
                                                           321
HUL33splice
          312 DFLQRMRQCFRGQLLDRRAFLRSQNNQRATAE
                                                           343
          237 DFVSKVGQCFRGELTNRRTFLRSKQQARNSDD
RhUL33
                                                           258
RhUL33splice 349
            [DFV|SK|V|G|QCFRG|E|LT|N|RRTFLRS|K|QQ|A|R|N|S|D|D
                                                           380
H UL33
            IT N L AAGNNSQSVATSLDTNSKNYNQHAKRS VS
                                                           353
HUL33splice
             TNLAAGNNSQSVATSLDTNSKNYNQHAKRSVS
                                                           375
             VIPIT I VSQQPI-IATPTI I VINKPEIKI - - INIPIHVKRGVS
RhUL33
          269
                                                           297
RhUL33splice 381
             <u>VPTIVSQQPI-ATPTIIVNKPEKI--NPHVKRGVS</u>
                                                           409
H UL33
            IF NFPSGTWKGGQKTASNDTSTKIPHRLSQSHH
                                                           385
            FNFPSGTWKGGQKTASNDTSTKIPHRLSQSHH
HUL33splice
          376
                                                           407
             |F|S|VSASS|EL|AA|A|K|A|KD|KA|-----K|RLS|M|SHQ
RhUL33
                                                           324
RhUL33splice 410
            FSVSASSELAAAKKAKDKA-
                                                           390
H UL33
          386 N L S GV
                                                           412
HUL33splice
            NLSGV
          408
                                                           329
RhUL33
             NLRLT
                                                           441
RhUL33splice 437
```



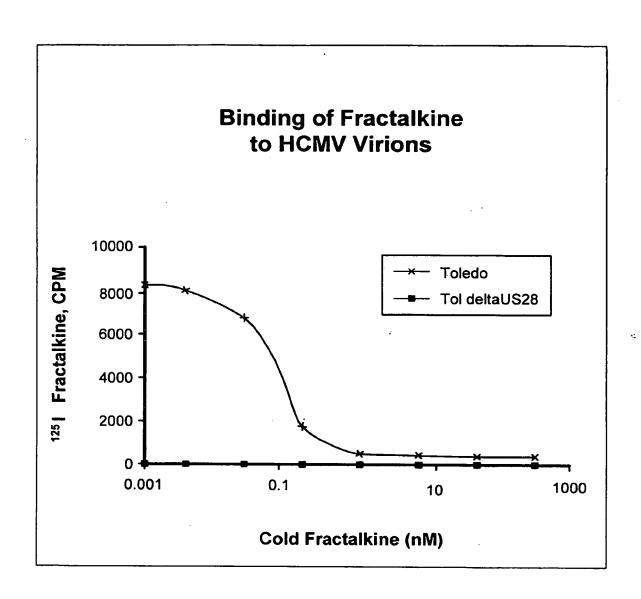


FIG. 5



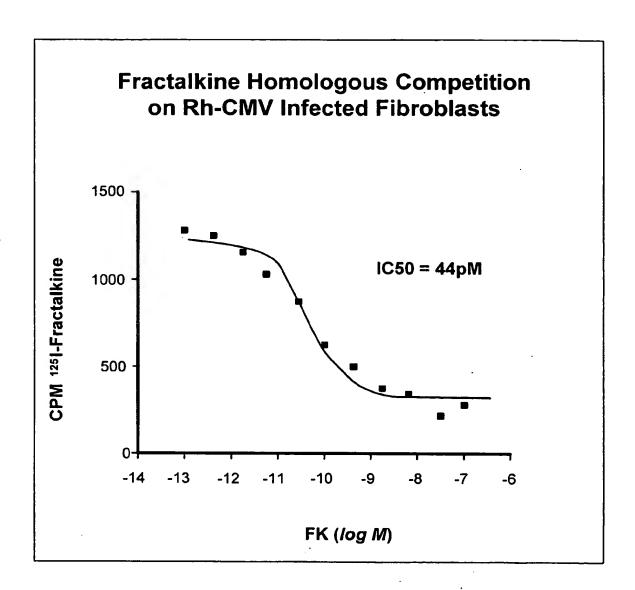


FIG. 6



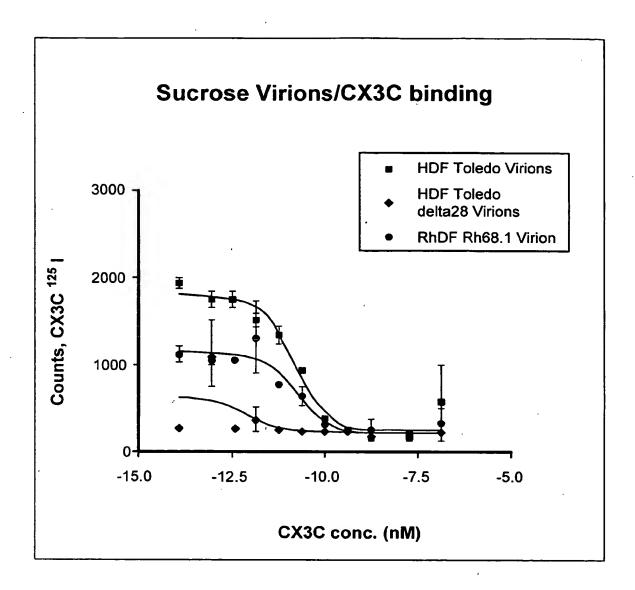


FIG. 7